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PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF
AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA
LNVPGSSSHDTLCTSGTFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLQLALEAPE
GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLQLALRVARMPGLERSVRERFLPVH

Fig. 1

09896096.052601

09896095.062301

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GTCCGCGCTGAGCCGCGCTCTCCCTGCTCCAGCAAGGACC
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GCAGAGACAGGGGAGCGGCTGGTGTGCGCCCACTGCCCCCAGGCACCTTTGTGCAGCGG
CCGTGCCGCGGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG
TTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGGGAGCGTGAGGAG
GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCTGCGCTGCCCGACCGGCTTCTTC
GCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCC
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CGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC
TGATCCTGGCCCCCTTTATTTATTCTACATCCTTGGCACCCCACTTGCACTGAAAGAGG
CTTTTTTTTAAATAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

Fig. 2

09395096-062801

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNNGG
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
GAACACGCAGTGCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT

Fig. 3

SEQ ID NO: 4 128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID NO: 5 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID NO: 6 1
 SEQ ID NO: 3 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 G
 SEQ ID NO: 4 178 CA-TTCTGGAACCTACCTGGAGCGC
 SEQ ID NO: 5 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCTCTGNGG
 SEQ ID NO: 6 2 CAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGG
 SEQ ID NO: 3 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCTCTGNGG
 SEQ ID NO: 5 101 GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAAACCGGCCT
 SEQ ID NO: 6 52 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAAACCGTGCCT
 SEQ ID NO: 7 1 GAGGGGCCCCAGGAGTGGTGGCCGGAGGTG
 SEQ ID NO: 3 101 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAAACCGTGCCT
 SEQ ID NO: 5 151 GCNGCTGCAGCACCGGNTTCTTCGCGCAGCGTGN¹TTCTGCTTGGAGCAC
 SEQ ID NO: 6 102 GCCGCTGCCGCACCGGCTTCTTCGCGCAGCGTGGTTTCTGCTTGGAGCAC
 SEQ ID NO: 7 32 TGGCAGGGGTCAGGTTGCTGGTCCCCAGCCTTGCAACCTGAGCTAGGACAC
 SEQ ID NO: 3 151 GCCGCTGCCGCACCGGCTTCTTCGCGCAGCGTGGTTTCTGCTTGGAGCAC
 SEQ ID NO: 5 201 GCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCACCCCCAGCCA
 SEQ ID NO: 6 152 GCATCGTGTCCACCTGGTGC CGCGGTGATTNCCCCGGGCACCCCCAGCCA
 SEQ ID NO: 7 82 CAGTCCCCCTGACCCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA
 SEQ ID NO: 8 1 GCATCGTGTCCACCTGGTGC CGCGGTGATTGCCCGGGACCCCCAGCCA
 SEQ ID NO: 10 1 CTGTCCACCTGGTGC CGCGGTGATTN¹CCC-GGGACCCCCAGCCA
 SEQ ID NO: 3 201 GCATCGTGTCCACCTGGTGC CGCGGTGATTGCCCGGGACCCCCAGCCA

Fig. 4

SEQ ID NO: 5 251 GAACACGCA - TGCAAAGCCGTG
 SEQ ID NO: 7 132 GAACACGCAGN - CC - AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 8 51 GAACACGCAG - GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 10 47 GAACACGCAGTGCC - AGCCNT - CCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 9 1 AGCNGTGCCNCCNAGGCACCTTCTCAGCCAGCAGT
 SEQ ID NO: 3 251 GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC

 SEQ ID NO: 7 182 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 8 101 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 10 97 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 9 36 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 3 301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT

 SEQ ID NO: 7 232 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAG
 SEQ ID NO: 8 151 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 10 147 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 9 86 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 3 351 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT

 SEQ ID NO: 10 197 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 9 136 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 3 401 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG

 SEQ ID NO: 10 247 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
 SEQ ID NO: 9 186 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
 SEQ ID NO: 3 451 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT

Fig. 4 (cont.)

UNA 10942
H1N1712

...MRALECPGISLLCLVIALPALIHVPAVRGVAIIDITYPWEDAEIG
MAPVAVWAAIAVGLLEWAAAHALPAQVAFIPYADPCGSEICRLREYVOOI

DNA 10942
H1NFR2

CRD1
15 ERLVCAQCPCPGTFVORPCRRDSPITTCGGPCPPRHYTOFWNYLERCRYCNVL
20 AOMCCSKCSPGONAKVFCIKISDTVCDSCEOSTYTOLWNWVPECCLSCGSR

DNA 10942
H1NFR2

CRD2
75 CGEREEEARACHATHNRACRCRTGFF...AHAG...FCLENASCPPGAGV
100 CSSDOVETQACTREONRICTCRPGWYCALSKOEGCRLCAPLRKCRPGFGV

DNA 10942
H1NFR2

CRD3
139 IAPGTFSQNTQCPGPPGTFSASSSSSEQCOPHRNCTALGLALNVPSSSS
150 ARPGETETSDVCKPCAPGTFSNTTSSSTOICRPHOICNVVA...IPGNAS

DNA 10942
H1NFR2

CRD4
189 KDTLCTSCGTGFPLSTRYPGAEECERAVIDFVAFODISIKRLORLLOALEA
196 RDAVCTSTST...PTRSMAPGAVNLPQVSTRSQNTOPTPEPSTAPSTSLL

DNA 10942
H1NFR2

229 PEGWGPPTP...RAGRAALOLKLRRRLTELLGAODGALLVRLLOALRVAMP
244 PMGPSPPAEGSTGDFALPVLIVGYTALGLLIIGVVMCVIMTQVKKPL

DNA 10942
H1NFR2

287 GLERSVREERFLPVH
293 CLOREAKVPHLPADKARGTQGPEQOHLITAPSSSSSSLESSASALORRA

H1NFR2

343 PTRNOPOAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD

H1NFR2

393 HSSOCSSQASSTMGDTSSSPSESPKDEQVPFSKEECAFRSOLETPETLLG

H1NFR2

443 STEEKPLPLGVPOAGMKPS

Fig. 5

09896096-062301

DcR3 1 M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A 31
 OPG 1 M N K L L C C A L V F L D I S I K W T T Q E T F P 25

CRD1

DcR3 32 E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C 62
 OPG 26 - . P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C 54

CRD2

DcR3 63 R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V 93
 OPG 55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P 85

CRD3

DcR3 94 L C G E R E E E A R A C H A T H N R A C R C R T G F F A H A G 124
 OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

CRD4

DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P 155
 OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

CRD5

DcR3 156 G T F S A S S S S E Q C Q P H R N C T A L G L A L N V P G S 186
 OPG 148 G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G N 178

CRD6

DcR3 187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D 217
 OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

CRD7

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R 247
 OPG 209 F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R 239

CRD8

DcR3 248 A G R A A L Q L K L R R R L T E L L G A Q D G A L - L V R L L 277
 OPG 240 I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I 270

CRD9

DcR3 278 Q A L R V A R M P G L E R S V R E R F L P V H 300
 OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

Fig. 6

SCANNED, # 14

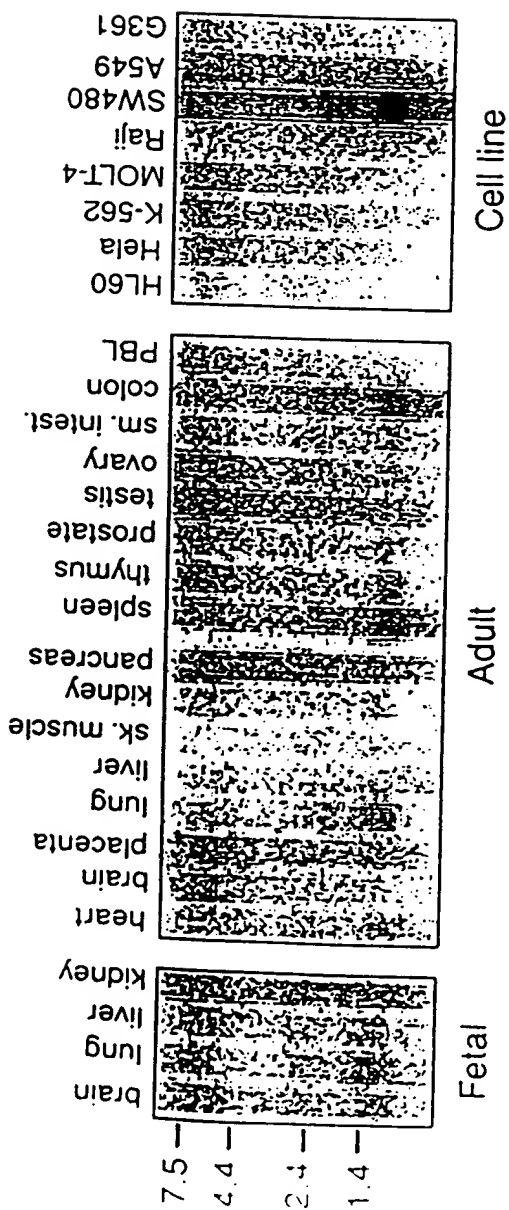


Fig. 7

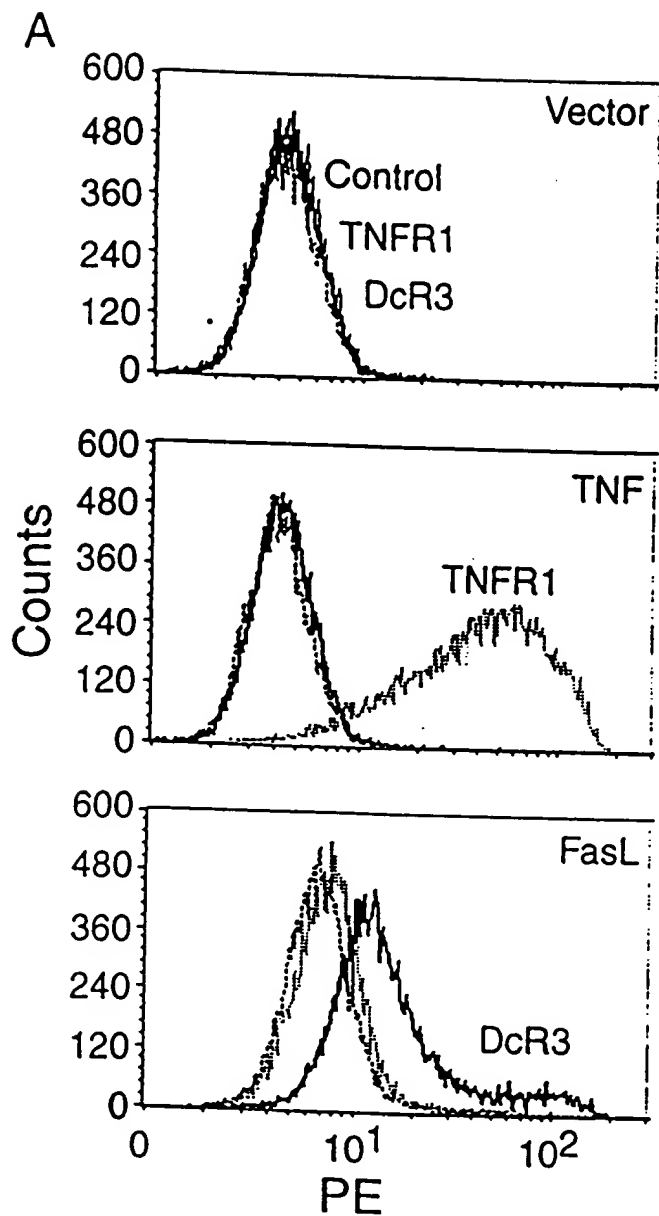
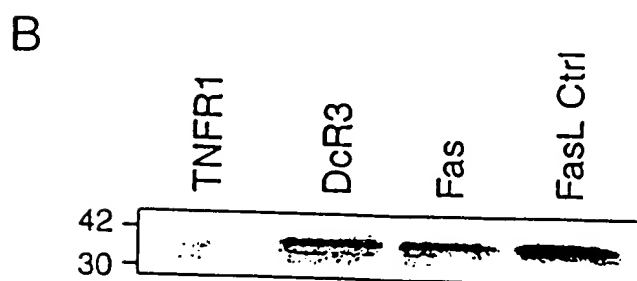


Fig. 8



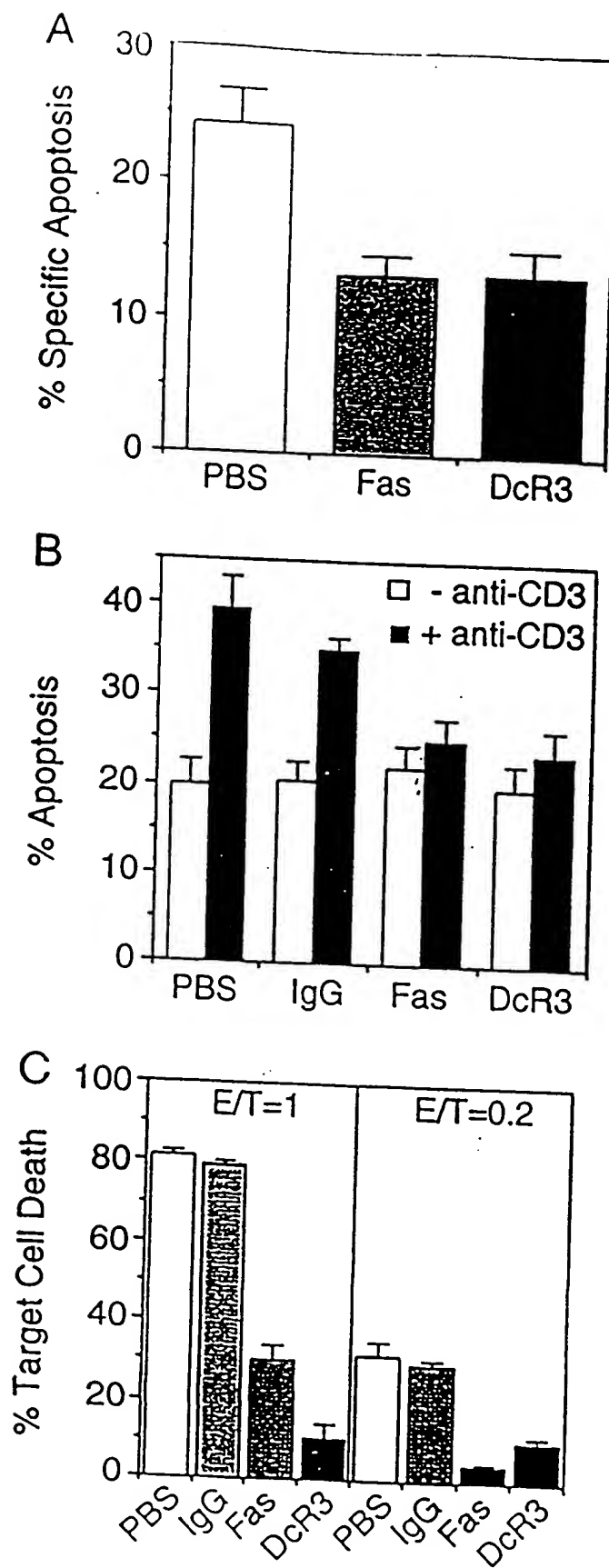


Fig. 9

103290" 96096860

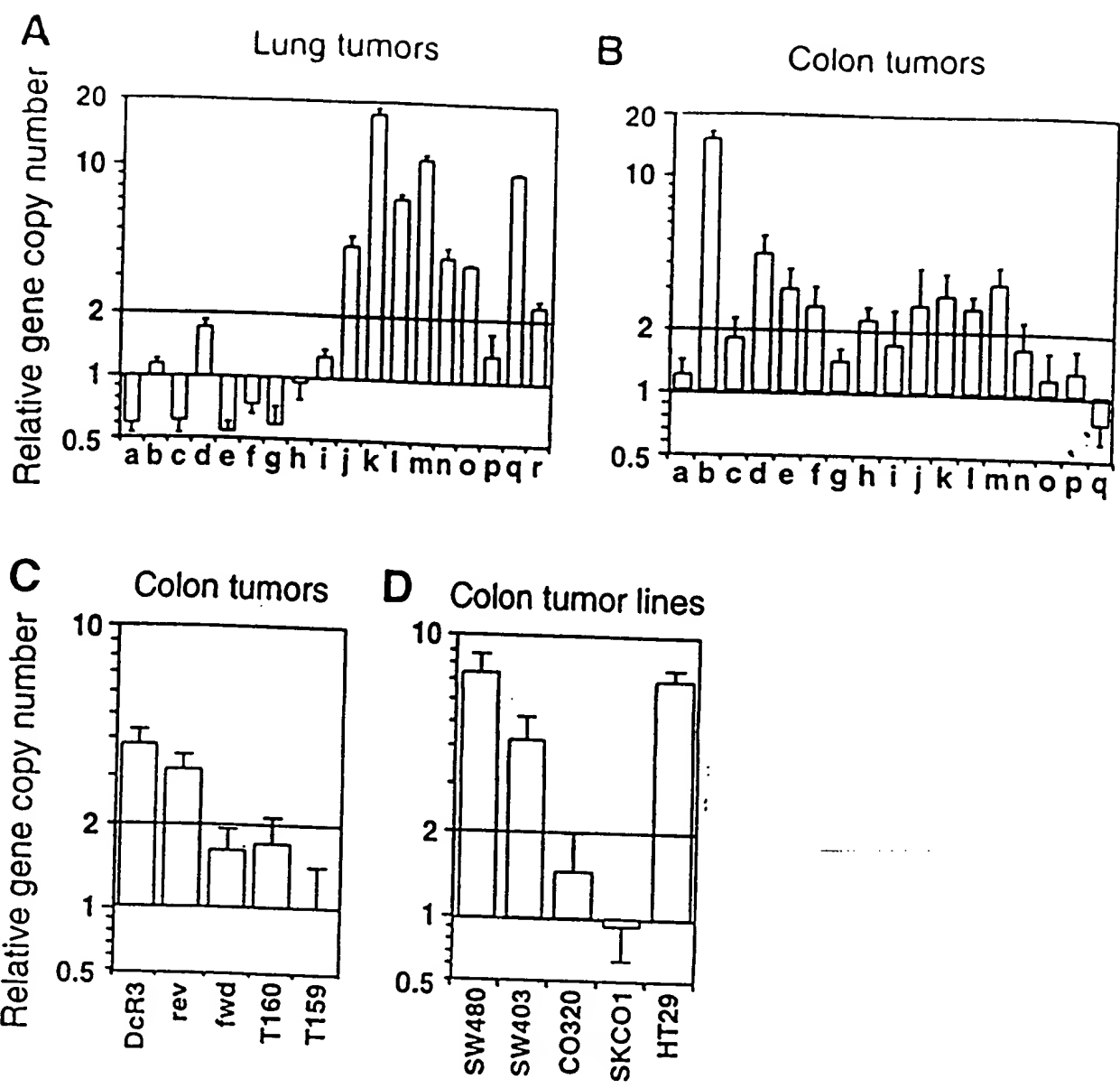


Fig. 10

00896099 06301
T08290" 96096860

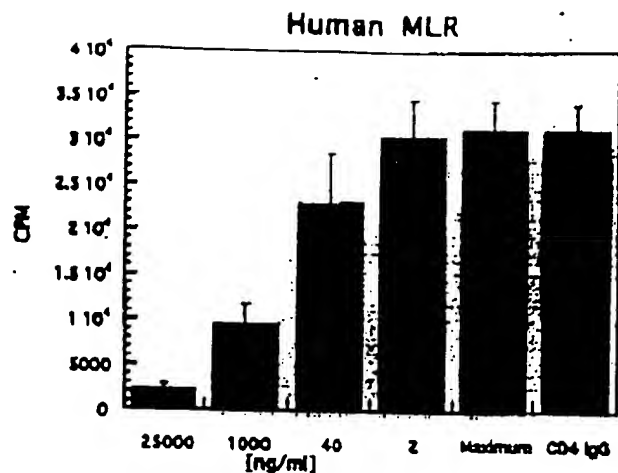


Fig. 11A

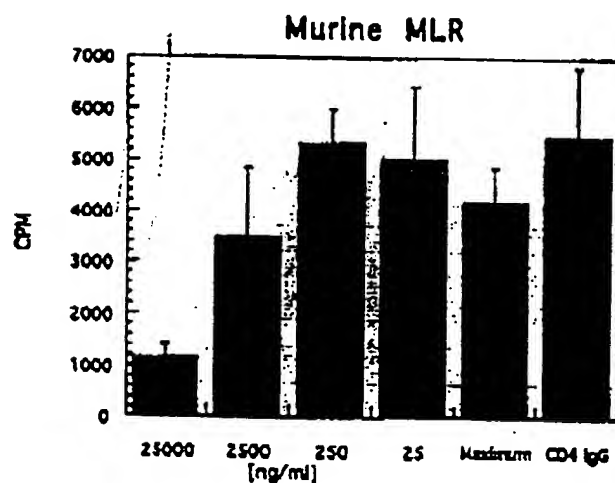


Fig. 11B

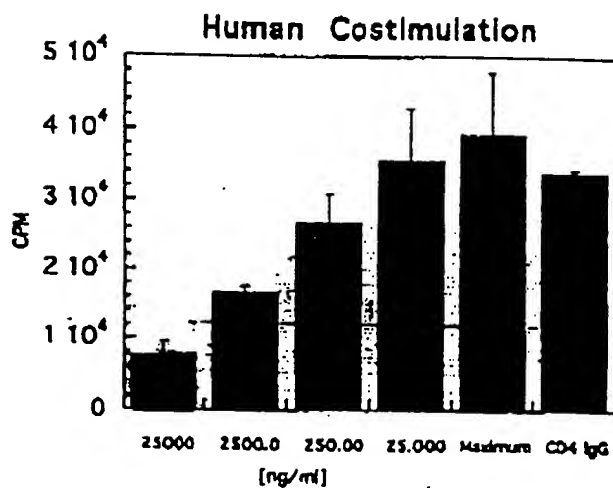


Fig. 11C

FIGURE 12

<u>mAb</u>	<u>Isotype</u>	<u>Antigen Specificity (ELISA)</u>					<u>% Blocking (ELISA)</u>
		<u>DcR3</u>	<u>DR4</u>	<u>DR5</u>	<u>DcR1</u>	<u>OPG</u>	
4B7.1.1	IgG1	+++	-	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.

% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

09896096-062801

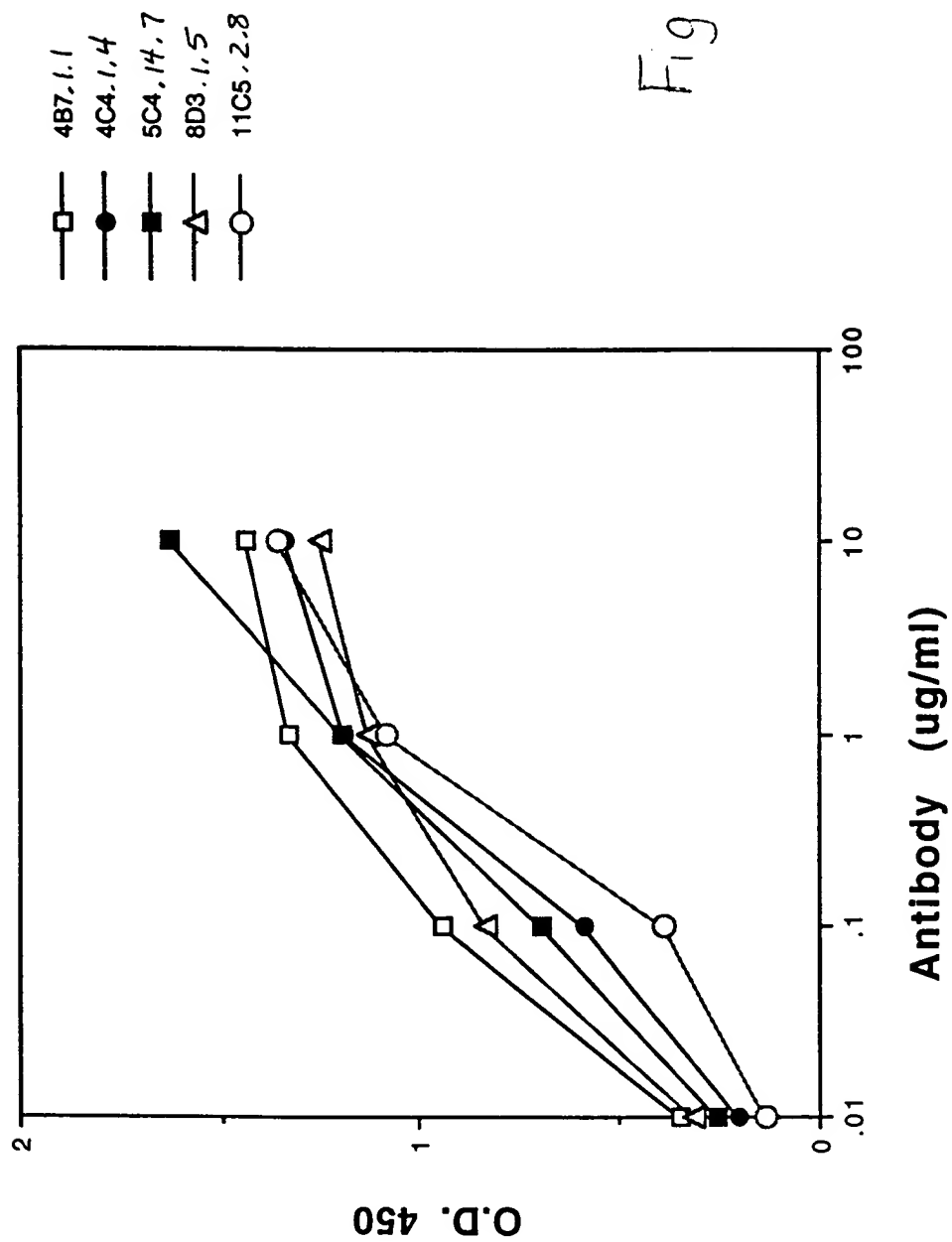


Fig. 13

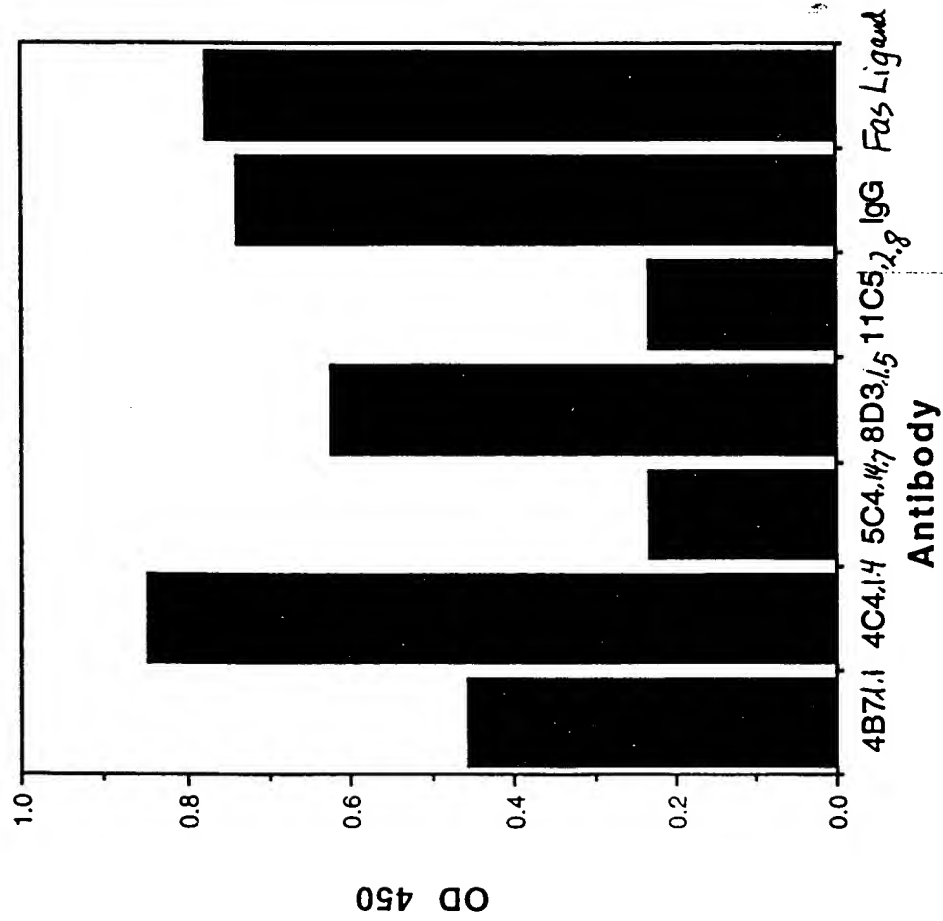


Fig. 14